Figure 1 Nucleotide Sequence of the 76kDa *C. pneumoniae* gene

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CDS 5'
(175)..(825)
CDS 3'
(940)..(2409)

ttgcggtgct gttaacggtg gagggcagtg tagtctgagc agtactcgtt gctgccgcgc 60

gcgccaccag acataatagc tgacagacta acagactgtt cctttccatg ggtcttttct 120

gcagtcaccg tcgtcgacac gtgtgatcag atatcgcggc cgctctagac cgcc atg   177
                                                          Met
                                                            1

aca aaa aaa cat tat gct tgg gtt gta gaa ggg att ctc aat cgt ttg   225
Thr Lys Lys His Tyr Ala Trp Val Val Glu Gly Ile Leu Asn Arg Leu
              5                  10                  15

cct aaa cag ttt ttt gtg aaa tgt agt gtt gtc gac tgg aac aca ttc   273
Pro Lys Gln Phe Phe Val Lys Cys Ser Val Val Asp Trp Asn Thr Phe
         20                  25                  30

gtt cct tca gaa acc tcc act aca gaa aaa gct gct aca aac gct atg   321
Val Pro Ser Glu Thr Ser Thr Thr Glu Lys Ala Ala Thr Asn Ala Met
     35                  40                  45

aaa tac aaa tac tgt gtt tgg cag tgg ctc gtc gga aag cat agt cag   369
Lys Tyr Lys Tyr Cys Val Trp Gln Trp Leu Val Gly Lys His Ser Gln
 50                  55                  60                  65

gtt cct tgg atc aat gga cag aaa aag cct cta tat ctt tat gga gct   417
Val Pro Trp Ile Asn Gly Gln Lys Lys Pro Leu Tyr Leu Tyr Gly Ala
                 70                  75                  80

ttc tta atg aac cct tta gca aag gct acg aag act acg tta aat gga   465
Phe Leu Met Asn Pro Leu Ala Lys Ala Thr Lys Thr Thr Leu Asn Gly
             85                  90                  95

aaa gaa aac cta gct tgg ttt att gga gga act tta ggg gga ctc aga   513
Lys Glu Asn Leu Ala Trp Phe Ile Gly Gly Thr Leu Gly Gly Leu Arg
        100                 105                 110

aaa gct gga gac tgg tct gcc aca gta cgt tat gag tat gtc gaa gcc   561
Lys Ala Gly Asp Trp Ser Ala Thr Val Arg Tyr Glu Tyr Val Glu Ala
    115                 120                 125

ttg tca gtt cca gaa ata gat gtt tca ggg att ggc cgt ggt aat tta   609
Leu Ser Val Pro Glu Ile Asp Val Ser Gly Ile Gly Arg Gly Asn Leu
130                 135                 140                 145

tta aag ttt tgg ttc gcc caa gca att gct gct aac tat gat cct aaa   657
Leu Lys Phe Trp Phe Ala Gln Ala Ile Ala Ala Asn Tyr Asp Pro Lys
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                150                     155                     160

gag gct aat agt ttt aca aat tat aaa gga ttt tcc gct cta tat atg    705
Glu Ala Asn Ser Phe Thr Asn Tyr Lys Gly Phe Ser Ala Leu Tyr Met
            165                     170                     175

tat ggc atc aca gat tct cta tca ttc aga gct tat ggg gct tac tcc    753
Tyr Gly Ile Thr Asp Ser Leu Ser Phe Arg Ala Tyr Gly Ala Tyr Ser
        180                     185                     190

aaa cca gca aac gat aaa ctc ggc agt gat ttt act ttc cga aag ttt    801
Lys Pro Ala Asn Asp Lys Leu Gly Ser Asp Phe Thr Phe Arg Lys Phe
    195                     200                     205

gat cta ggt ata att tca gcg ttt taagtcaaat tttaataaaa tctttaaaaa   855
Asp Leu Gly Ile Ile Ser Ala Phe
210                     215

caggctcgca ttaattatta gtgagagctt tttttttatt ttttataata aaactaaaag 915

atttttatta tttttgagtt tttt atg gtt aat cct att ggt cca ggt cct     966
                           Met Val Asn Pro Ile Gly Pro Gly Pro
                                       220                     225

ata gac gaa aca gaa cgc aca cct ccc gca gat ctt tct gct caa gga    1014
Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu Ser Ala Gln Gly
            230                     235                     240

ttg gag gcg agt gca gca aat aag agt gcg gaa gct caa aga ata gca    1062
Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala Gln Arg Ile Ala
        245                     250                     255

ggt gcg gaa gct aag cct aaa gaa tct aag acc gat tct gta gag cga    1110
Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp Ser Val Glu Arg
    260                     265                     270

tgg agc atc ttg cgt tct gca gtg aat gct ctc atg agt ctg gca gat    1158
Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met Ser Leu Ala Asp
275                     280                     285                     290

aag ctg ggt att gct tct agt aac agc tcg tct tct act agc aga tct    1206
Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser Thr Ser Arg Ser
                295                     300                     305

gca gac gtg gac tca acg aca gcg acc gca cct acg cct cct cca ccc    1254
Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr Pro Pro Pro Pro
            310                     315                     320

acg tct gat gat tat aag act caa gcg caa aca gct tac gat act atc    1302
Thr Ser Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala Tyr Asp Thr Ile
        325                     330                     335

ttt acc tca aca tca cta gct gac ata cag gct gct ttg gtg agc ctc    1350
Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala Leu Val Ser Leu
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    340                 345                 350

cag gat gct gtc act aat ata aag gat aca gcg gct act gat gag gaa    1398
Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala Thr Asp Glu Glu
355                 360                 365                 370

acc gca atc gct gcg gag tgg gaa act aag aat gcc gat gca att aaa    1446
Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala Asp Ala Ile Lys
                375                 380                 385

gtt ggc gcg caa att aca gaa tta gcg aaa tat gct tcg gat aac caa    1494
Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala Ser Asp Asn Gln
            390                 395                 400

gcg att ctt gac tct tta ggt aaa ctg act tcc ttc gac ctc tta cag    1542
Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe Asp Leu Leu Gln
        405                 410                 415

act gct ctt ctc caa tct gta gca aac aat aac aaa gca gct gag ctt    1590
Thr Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys Ala Ala Glu Leu
    420                 425                 430

ctt aaa gag atg caa gat aac cca gta gtc cca ggg aaa acg cct gca    1638
Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly Lys Thr Pro Ala
435                 440                 445                 450

att gct caa tct tta gtt gat cag aca gat gct aca gcg aca cag ata    1686
Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr Ala Thr Gln Ile
                455                 460                 465

gag aaa gat gga aat gcg att ggg gat gca tat ttt gca gga cag aac    1734
Glu Lys Asp Gly Asn Ala Ile Gly Asp Ala Tyr Phe Ala Gly Gln Asn
            470                 475                 480

gct agt gga gct gta gaa aat gct aaa tct aat aac agt ata agc aac    1782
Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn Ser Ile Ser Asn
        485                 490                 495

ata gat tca gct aaa gca gca atc gct act gct aag aca caa ata gct    1830
Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys Thr Gln Ile Ala
    500                 505                 510

gaa gct cag aaa aag ttc ccc gac tct cca att ctt caa gaa gcg gaa    1878
Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu Gln Glu Ala Glu
515                 520                 525                 530

caa atg gta ata cag gct gag aaa gat ctt aaa aat atc aaa cct gca    1926
Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn Ile Lys Pro Ala
                535                 540                 545

gat ggt tct gat gtt cca aat cca gga act aca gtt gga ggc tcc aag    1974
Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val Gly Gly Ser Lys
            550                 555                 560
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caa caa gga agt agt att ggt agt att cgt gtt tcc atg ctg tta gat   2022
Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser Met Leu Leu Asp
        565                 570                 575

gat gct gaa aat gag acc gct tcc att ttg atg tct ggg ttt cgt cag   2070
Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser Gly Phe Arg Gln
    580                 585                 590

atg att cac atg ttc aat acg gaa aat cct gat tct caa gct gcc caa   2118
Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser Gln Ala Ala Gln
595                 600                 605                 610

cag gag ctc gca gca caa gct aga gca gcg aaa gcc gct gga gat gac   2166
Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala Ala Gly Asp Asp
                615                 620                 625

agt gct gct gca gcg ctg gca gat gct cag aaa gct tta gaa gcg gct   2214
Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala Leu Glu Ala Ala
            630                 635                 640

cta ggt aaa gct ggg caa caa cag ggc ata ctc aat gct ttg gga cag   2262
Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn Ala Leu Gly Gln
        645                 650                 655

atc gct tct gct gct gtt gtg agc gca gga gtc ctc ccg ctg cag caa   2310
Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val Leu Pro Leu Gln Gln
    660                 665                 670

gtt cta tgg atc cga gct cgg tac caa gct tac gta gaa caa aaa ctc   2358
Val Leu Trp Ile Arg Ala Arg Tyr Gln Ala Tyr Val Glu Gln Lys Leu
675                 680                 685            Myc  690

atc tca gaa gag gat ctg aat agc gcc gtc gac cat cat cat cat cat   2406
Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His His
                695                 700            His 705

cat tgagtttaaa cggtctccag cttaagttta aaccgctgat cagcctcgac        2459
His

tgtgccttct agttgccagc catctgttgt ttgcccctcc cccgtgcctt ccttgaccct 2519

ggaaggtgcc actcccactg tccttt                                      2545
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Figure 2 Construction of pCAD76kDa

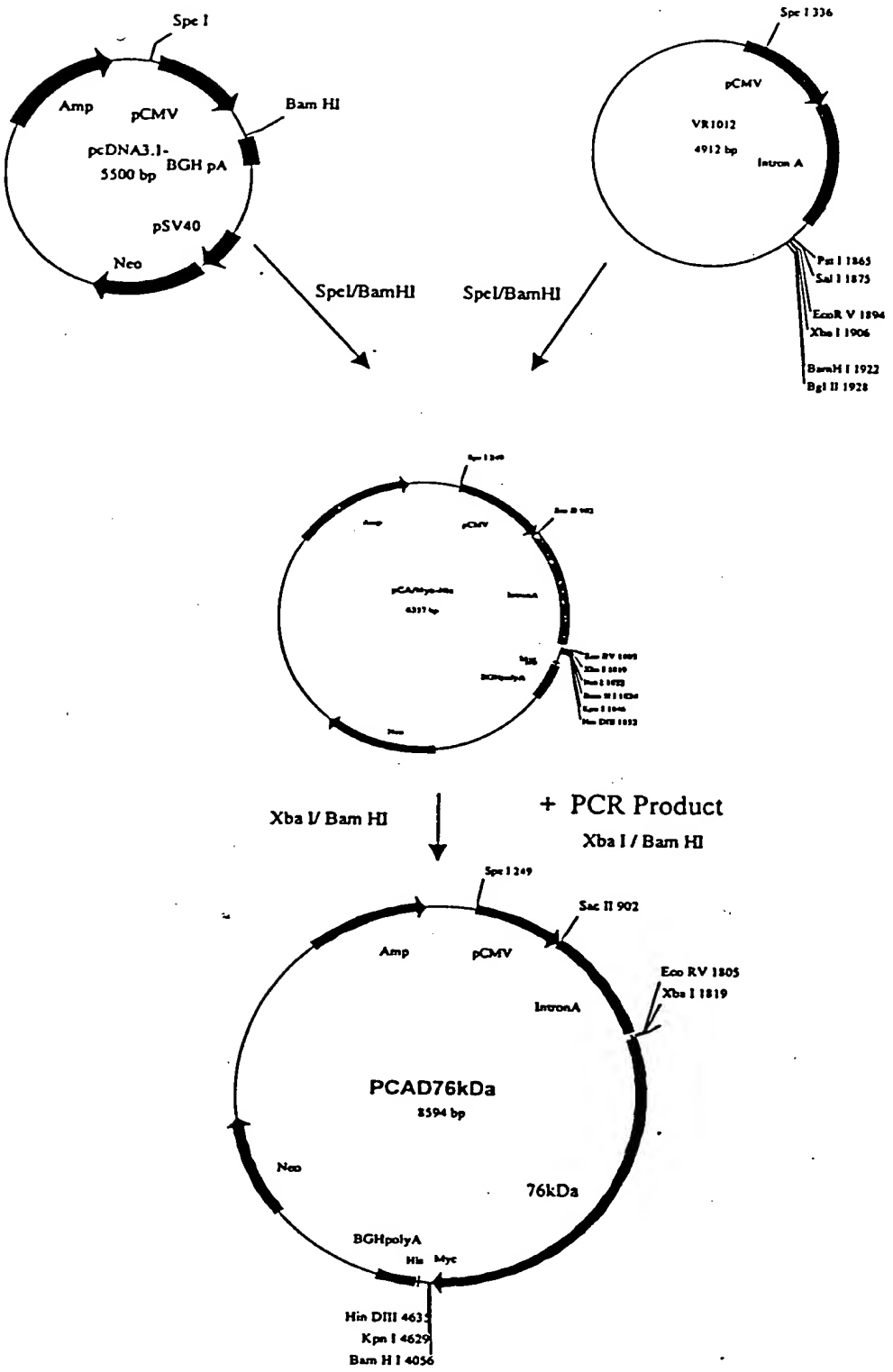

Figure 3 Nucleotide sequence of the *C. pneumoniae* MOMP gene.

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(126)..(1307)

tgagcagtac tcgttgctgc cgcgcgcgcc accagacata atagctgaca gactaacaga 60

ctgttccttt ccatgggtct tttctgcagt caccgtcgtc gacacgtgtg atcagatatc 120

ccacc atg ttg cct gta ggg aac cct tct gat cca agc tta tta att gat 170
      Met Leu Pro Val Gly Asn Pro Ser Asp Pro Ser Leu Leu Ile Asp
        1               5                  10                  15

ggt aca ata tgg gaa ggt gct gca gga gat cct tgc gat cct tgc gct   218
Gly Thr Ile Trp Glu Gly Ala Ala Gly Asp Pro Cys Asp Pro Cys Ala
                20                  25                  30

act tgg tgc gac gct att agc tta cgt gct gga ttt tac gga gac tat   266
Thr Trp Cys Asp Ala Ile Ser Leu Arg Ala Gly Phe Tyr Gly Asp Tyr
            35                  40                  45

gtt ttc gac cgt atc tta aaa gta gat gca cct aaa aca ttt tct atg   314
Val Phe Asp Arg Ile Leu Lys Val Asp Ala Pro Lys Thr Phe Ser Met
        50                  55                  60

gga gcc aag cct act gga tcc gct gct gca aac tat act act gcc gta   362
Gly Ala Lys Pro Thr Gly Ser Ala Ala Ala Asn Tyr Thr Thr Ala Val
    65                  70                  75

gat aga cct aac ccg gcc tac aat aag cat tta cac gat gca gag tgg   410
Asp Arg Pro Asn Pro Ala Tyr Asn Lys His Leu His Asp Ala Glu Trp
80                  85                  90                  95

ttc act aat gca ggc ttc att gcc tta aac att tgg gat cgc ttt gat   458
Phe Thr Asn Ala Gly Phe Ile Ala Leu Asn Ile Trp Asp Arg Phe Asp
                100                 105                 110

gtt ttc tgt act tta gga gct tct aat ggt tac att aga gga aac tct   506
Val Phe Cys Thr Leu Gly Ala Ser Asn Gly Tyr Ile Arg Gly Asn Ser
            115                 120                 125

aca gcg ttc aat ctc gtt ggt tta ttc gga gtt aaa ggt act act gta   554
Thr Ala Phe Asn Leu Val Gly Leu Phe Gly Val Lys Gly Thr Thr Val
        130                 135                 140

aat gca aat gaa cta cca aac gtt tct tta agt aac gga gtt gtt gaa   602
Asn Ala Asn Glu Leu Pro Asn Val Ser Leu Ser Asn Gly Val Val Glu
    145                 150                 155

ctt tac aca gac acc tct ttc tct tgg agc gta ggc gct cgt gga gcc   650
Leu Tyr Thr Asp Thr Ser Phe Ser Trp Ser Val Gly Ala Arg Gly Ala
160                 165                 170                 175
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tta tgg gaa tgc ggt tgt gca act ttg gga gct gaa ttc caa tat gca   698
Leu Trp Glu Cys Gly Cys Ala Thr Leu Gly Ala Glu Phe Gln Tyr Ala
                180                 185                 190

cag tcc aaa cct aaa gtt gaa gaa ctt aat gtg atc tgt aac gta tcg   746
Gln Ser Lys Pro Lys Val Glu Glu Leu Asn Val Ile Cys Asn Val Ser
            195                 200                 205

caa ttc tct gta aac aaa ccc aag ggc tat aaa ggc gtt gct ttc ccc   794
Gln Phe Ser Val Asn Lys Pro Lys Gly Tyr Lys Gly Val Ala Phe Pro
        210                 215                 220

ttg cca aca gac gct ggc gta gca aca gct act gga aca aag tct gcg   842
Leu Pro Thr Asp Ala Gly Val Ala Thr Ala Thr Gly Thr Lys Ser Ala
    225                 230                 235

acc atc aat tat cat gaa tgg caa gta gga gcc tct cta tct tac aga   890
Thr Ile Asn Tyr His Glu Trp Gln Val Gly Ala Ser Leu Ser Tyr Arg
240                 245                 250                 255

cta aac tct tta gtg cca tac att gga gta caa tgg tct cga gca act   938
Leu Asn Ser Leu Val Pro Tyr Ile Gly Val Gln Trp Ser Arg Ala Thr
                260                 265                 270

ttt gat gct gat aac atc cgc att gct cag cca aaa cta cct aca gct   986
Phe Asp Ala Asp Asn Ile Arg Ile Ala Gln Pro Lys Leu Pro Thr Ala
            275                 280                 285

gtt tta aac tta act gca tgg aac cct tct tta cta gga aat gcc aca   1034
Val Leu Asn Leu Thr Ala Trp Asn Pro Ser Leu Leu Gly Asn Ala Thr
        290                 295                 300

gca ttg tct act act gat tcg ttc tca gac ttc atg caa att gtt tcc   1082
Ala Leu Ser Thr Thr Asp Ser Phe Ser Asp Phe Met Gln Ile Val Ser
    305                 310                 315

tgt cag atc aac aag ttt aaa tct aga aaa gct tgt gga gtt act gta   1130
Cys Gln Ile Asn Lys Phe Lys Ser Arg Lys Ala Cys Gly Val Thr Val
320                 325                 330                 335

gga gct act tta gtt gat gct gat aaa tgg tca ctt act gca gaa gct   1178
Gly Ala Thr Leu Val Asp Ala Asp Lys Trp Ser Leu Thr Ala Glu Ala
                340                 345                 350

cgt tta att aac gag aga gct gct cac gta tct ggt cag ttc aga ttc   1226
Arg Leu Ile Asn Glu Arg Ala Ala His Val Ser Gly Gln Phe Arg Phe
            355                 360                 365

cgg tac caa gct tac gta gaa caa aaa ctc atc tca gaa gag gat ctg   1274
Arg Tyr Gln Ala Tyr Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
        370                 375         Myc     380

aat agc gcc gtc gac cat cat cat cat cat cat tgagtttaaa cggtctccag 1327
Asn Ser Ala Val Asp His His His His His His
                                    His
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385 390

cttaagttta aaccgctgat cagcctcgac tgtgccttct agttgccagc catctgttgt 1387

ttgcccctcc cccgtgcctt ccttgaccct ggaaggtgc 1426

Figure 4 Construction of pCAMOMP

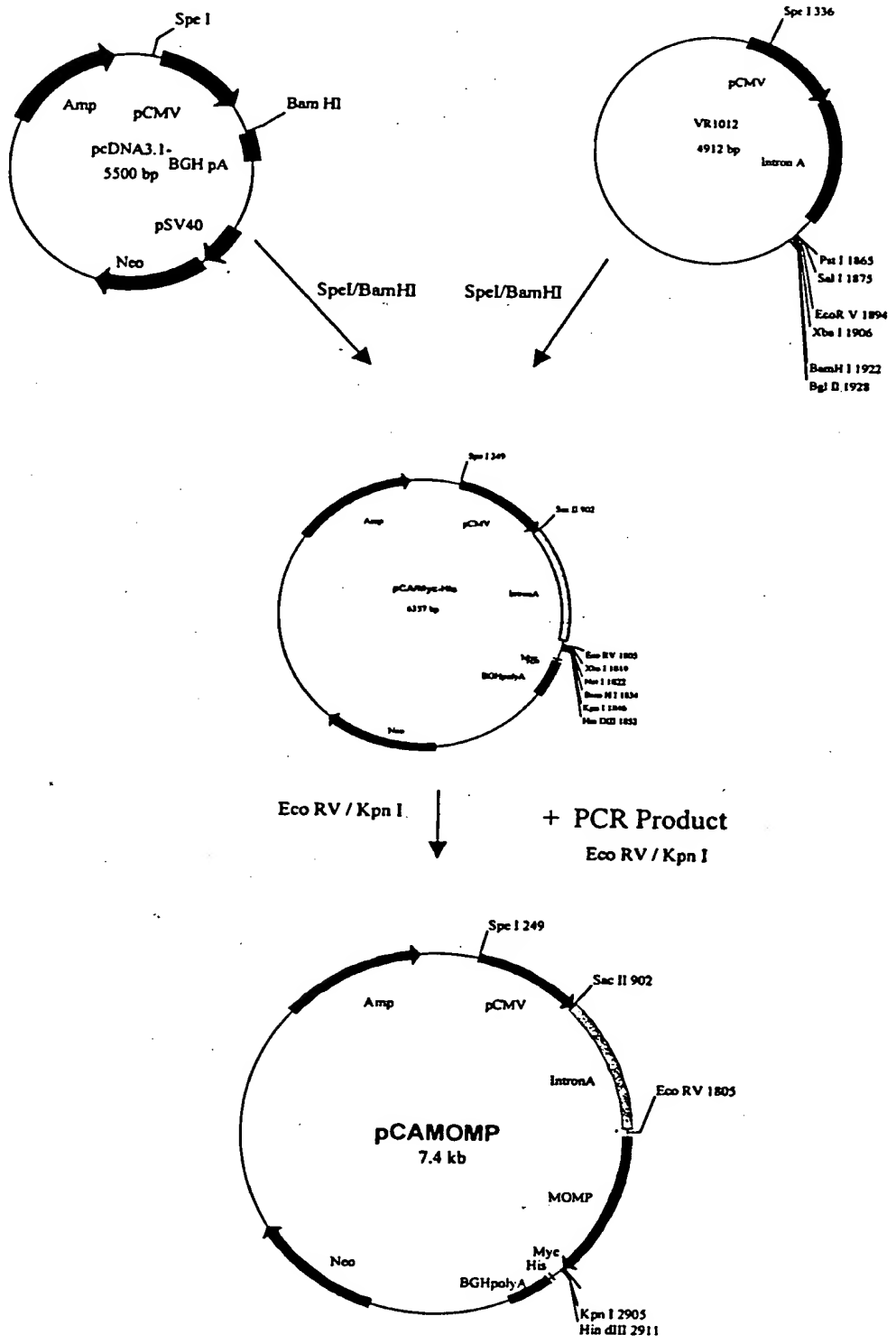

Fig 5